

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH MUS MUSCULUS INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN SEQ IN NO:13

Query: IGFBP_like protein (SEQ ID NO: 6)

Subject: >gi|9055246 (AB006141) IGFBP-like protein [Mus musculus] SEQ ID NO: 13

Length = 270

Score = 1170 (416.9 bits), Expect = 1.8e-118, p = 1.8e-118

Identities = 209/269 (77%), Positives = 232/269 (86%)

Query: 8 LPLLLLLLPLPLPSLGI RDVGRRPKCGPCRPEGCPAPAPCPAPGISALDEGCCA 67

+P L LLLL LLP L+ LG+RD G R P+C PC+ + CPAP+PCPAP ISA DECGCCA

1 MPRLPLLLL-LLPSLARGGLRDAGRHRHECSPCQQRCPAPSPCPAPWISARDECGCCA 59

Query: 68 RCLGAEGASCGRAGRCGPGLVCASQAAGAAPEGTGLCVCAQRGTVCGSDGRSYPVCA 127

RCLGAEGASCGG G RCGPGLVCAS+A+G APEGTGLCVCAQRG VCGSDGRSY S+CA

Sbjct: 60 RCLGAEGASCGPVGSRGCGPLVCASRASGTAPEGTGLCVCAQRGAVCGSDGRSYSSICA 119

Query: 128 LRLRARHTPRAHPGHLHKARDGPFAPVVVVPPRSVHNVTGAQVGLSCEVRAVPTPVIT 187

LRLRARH PRAH GHILKARDGCEFAVV++PPR +HNVTG QV LSCEV+AVTTPVIT

Sbjct: 120 LRLRARHAPRAHHGLHKARDGPCFAPVVLMPPRDIHNVGTGTQVFLSCEVKA VPTPVIT 179

Query: 188 WRKVTKSPEGTQALEELPGDHVNIAVQVRGGPSDHEATAWILINPLRKEDEGVYQCHAAN 247

W+KV SPECT+ LEELPGDHVNIAVQVRGGPSDHE T+WILINPLRKEDEGVY CHAAN

Sbjct: 180 WKKVKHSPGTEGLEELPGDHNIAVQVRGGPSDHTTWSWILINPLRKEDEGVYHCHAAN 239

Query: 248 MVGEAESHSTVTVLDLSKYRSFHFPAPDD 276

+GEA+SH TVTVL_{DL}+Y+S + P D

Sbjct: 240 AIGEAQSHGTVTVLDLNRYKSLYSSVPGD 268

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 6 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN-LIKE POLYPEPTIDE (IDENTIFIED AS IGFBP-7-HY1) WITH HOMO SAPIENS PROSTOGLANDIN I2 SEQ NO:14

Query: IGFBP_like protein (SEQ ID NO: 6)
 Subject: >gi|1082724 prostoglandin I2 [Homo sapiens (SEQ ID NO: 14)]
 Length: 273

Score = 570 (205.7 bits), Expect = 7.9e-61, P = 7.9e-61
 Identities = 123/273 (45%), Positives = 150/273 (54%)

Query:	4	PSLRALLGAAGLLLLLL--PLSSSS-SDT-----CGPCEPASCPLPLGCLLGETR	54
		P L +LLL LLLL L PLS S D CGPC P CP P	
Sbjct:	2	PRL-SLLPLLLLLLLPLPLPSLGI RDVGRRPKCGPCRPEGCPAPAPCAPGISAL	60
Query:	55	DACGCCPMARGEPEPCGGGAGRGYCAPMECVKSRKRKKGAGAAAGPGVSGVCVK	114
		D CGCC C EG CGG GR C PG+ C AGAA G +G+CVC	
Sbjct:	61	DECGCCARCLGAEGASCGRAGGR--CGPGLVCASQA-----AGAAPEG--TGLCVCA	109
Query:	115	SRYPVCGSDGTTYPSCQLRAASQRAESRGEKAITQVSKGTCEQGPSIVTPPKDIWNV	174
		R VCGSDG +YPS C LR ++ + + G CE P +V PP+ + NVTG	
Sbjct:	110	QRTVCGSDGRSYPVSVCALRLRARHTPRAHPGHLHKARDGPCEFAFVVPVPPRSVHNVTG	169
Query:	175	AQVYLSCEVIGIPTPVLINWKVRGHYGVQRTPELLPGDRDNLAIQTRGGPEKHEVTGWVL	234
		AQV LSCEV +PTPV+ W KV + G Q E LPGD N+A+Q RGGP HE T W+L	
Sbjct:	170	AQVGLSCEVRAVPTPVITWRKVTKSPEGTQALEELPGDHVNIAVQVRGGPSDHEATAWIL	229
Query:	235	VSPLSKEDAGEYECHASNSQGOASASAKITVVD	267
		++PL KED G Y+CHA+N G+A + + +TV+D	
Sbjct:	230	INPLRKEDEGVYQCHAANMVGEAESHSTVTVLD	262

FIG. 2